

SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.
 SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.
 SEQ ID NO: 3 is primate DCRS6 reverse translation.
 SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.
 SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.
 SEQ ID NO: 6 is rodent DCRS6 reverse translation.
 SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.
 SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.
 SEQ ID NO: 9 is primate DCRS7 reverse translation.
 SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.
 SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.
 SEQ ID NO: 12 is rodent DCRS7 reverse translation.
 SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.
 SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.
 SEQ ID NO: 15 is primate DCRS8 reverse translation.
 SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.
 SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.
 SEQ ID NO: 18 is primate DCRS9 reverse translation.
 SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.
 SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.
 SEQ ID NO: 21 is rodent DCRS9 reverse translation.
 SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.
 SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.
 SEQ ID NO: 24 is primate DCRS10 reverse translation.
 SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.
 SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.
 SEQ ID NO: 27 is rodent DCRS10 reverse translation.
 SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.
 SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.
 SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.
 SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

<110> Gorman, Daniel M.

<120> Mammalian Receptor Proteins; Related Reagents and Methods

<130> DX01170K US

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<150> US 60/206,862

<151> 2000-05-24

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

<211> 1796

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: primate; surmised
Homo sapiens

09863818.052301

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<220>
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 <222> (46)..(1509)

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Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser	
5 10 15	
cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac	144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp	
20 25 30	
ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca	192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser	
35 40 45	
att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc	240
Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg	
50 55 60 65	
ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag	288
Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln	
70 75 80	
tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag	336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln	
85 90 95	
acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct	384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro	
100 105 110	
gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat	432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn	
115 120 125	
gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca	480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser	
130 135 140 145	
cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag	528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys	
150 155 160	
gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag	576
Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu	
165 170 175	
gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac	624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr	
180 185 190	

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Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe	
195 200 205	
gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca gtg	720
Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val	
210 215 220 225	
act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt cct	768
Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro	
230 235 240	
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Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys	
245 250 255	
cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag ccg	864
Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro	
260 265 270	
gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg	912
Gly Gly Trp Leu Pro Leu Leu Leu Ser Leu Leu Val Ala Thr Trp	
275 280 285	
gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc aag	960
Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys	
290 295 300 305	
aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt ctt	1008
Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu	
310 315 320	
gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac ttc	1056
Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe	
325 330 335	
act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag	1104
Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys	
340 345 350	
tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc	1152
Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala	
355 360 365	
act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac	1200
Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp	
370 375 380 385	
gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc	1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro	
390 395 400	
agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc	1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys	
405 410 415	
agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac	1344
Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr	
420 425 430	

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ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc 1392
 Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
 435 440 445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt 1440
 Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
 450 455 460 465

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc 1488
 Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
 470 475 480

cac gat ggc tgc tgc tcc ttg tagccacccc atgagaagca agagacotta 1539
 His Asp Gly Cys Cys Ser Leu
 485

aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgaccta agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatata caataaaatt ttcaaataatt 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

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ataaagcatc ttcagcc 1796

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<213> Unknown

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Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 20 25 30

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 35 40 45 50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 55 60 65

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 70 75 80

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 85 90 95

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 100 105 110

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 115 120 125 130

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Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro
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Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala
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Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu
			165				170						175		
Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met
			180				185						190		
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Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr
					215					220				225	
Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr
			230						235					240	
Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro
			245					250					255		
Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly
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Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	Val
			310					315						320	
Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	Thr
			325					330					335		
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Gln	Lys	Lys	Ala	Ala	Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val
					375					380				385	
Asn	Ser	Val	Cys	Asp	Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Ser
			390					395						400	
Glu	Asn	Ser	Gln	Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser
			405					410					415		
Asp	Leu	Arg	Ser	Gln	Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe
						425						430			
Arg	Glu	Ile	Asp	Thr	Lys	Asp	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro
						440					445				450

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
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Asp Gly Cys Cys Ser Leu
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 <213> reverse translation

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 athccngngg ayytnmgnga yytnmgngtn garccngtna cnacnwsngt ngcnacnggn 180
 gaytaywsna thytnatgaa ygtwnsntgg gtntnmgng cngaygcnws nathmgnytn 240
 ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300
 mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsnggngg naartggacn 360
 ttywsntaya thggnttycc ngtngarytn aayacngtnt ayttyathgg ngcncaayaay 420
 athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480
 ggntgyytnng aycayathat gaartayaar aaraartgyg tnaargcngg nwsnytnntgg 540
 gayccnaaya thacngcntg yaaraaraay gargaracng tngargtnaa yttyacnacn 600
 acncnnytnng gnaaymgnta yatggcnytn athcarcayw snacnathat hggnttywsn 660
 cargtnnttyg arcncayca raaraarcar acnmngncnw sngtnngtnat hccngtnacn 720
 ggngaywsng arggngcnac ngtnrcarytn acncntayt tyccnacntg yggnwsngay 780
 tgyathmgnc ayaarggnac ngtnngnytn tgyccncara cnggngtncc nttyccnytn 840
 gayaayaaya arwsnaarcc nggnggntgg ytnccnytny tnytnytnws nytnytnngtn 900
 gcnacntggg tnytngtngc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960
 acnwsnttyw snacnacnac nytnytnccn ccnathaarg tnytngtngt ntayccnwsn 1020
 garathtgyt tycaycayac nathtgytay ttyacngart tyytncaraa ycaytgymgn 1080
 wsngargtna thytngaraa rtggcaraar aaraarathg cngaratggg nccngtncar 1140

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tggytngcna cncaraaraa rgcngcngay aargtngtnt tyytnytnws naaygaygtn 1200
 aaywsngtnt gygayggnac ntgyggnaar wsnrggggnw snccnwsnga raaywsncar 1260
 gayytnttyc cnytngcntt yaayytntty tgywsngayy tnmgnwsnca rathcayytn 1320
 cayaartayg tngtngtnta yttymngnar athgayacna argaygayta yaaygcnytn 1380
 wsngtntgye cnaartayca yytnatgaar gaygcnacng cnttytgygc ngarytnytn 1440
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 ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc 96
 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
 20 25 30
 caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc 144
 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
 35 40 45
 aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat 192
 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
 50 55 60
 gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa 240
 Asp Ser Cys Ser Pro Leu
 65 70

gccttcctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag 300
 aggctgtgtg gaggtagtgc tatgtacaaa cttgctttaa aactggagtt tgcaaagtca 360
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 agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac 480
 tgagaaccac gcactctggc catgaggtaa tacggcactt ccctgtcagg ctgtctgtca 540
 gggtgggtct gtcttgcaat gcccatgctc tatgctgcac gtagaccgtt ttgtaacatt 600

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637

<210> 5
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 <212> PRT
 <213> Unknown

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 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
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 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
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 acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180
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 <212> DNA
 <213> Unknown

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 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
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 <220>

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<221> mat_peptide
<222> (241)..(2289)

<220>
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<222> (664)
<223> Xaa translation depends on genetic code

<400> 7

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tctgcccccc ttggggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180

atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20 -15 -10 -5

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Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
-1 1 5 10

tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc 324
Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
15 20 25

ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg 372
Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
30 35 40

cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt 420
His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60

gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75

gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg 516
Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90

gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc 564
Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105

ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg 612
Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Glu Glu Val Gln Val
110 115 120

cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat 660
Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125 130 135 140

gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat 708
Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
145 150 155

act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct 756

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 Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
 175 180 185
 ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt 852
 Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val
 190 195 200
 ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat 900
 Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn
 205 210 215 220
 cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga 948
 Gln Val Gln Gly Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly
 225 230 235
 ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt 996
 Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys
 240 245 250
 att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc 1044
 Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys
 255 260 265
 ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc 1092
 Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala
 270 275 280
 cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc 1140
 Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys
 285 290 295 300
 tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac 1188
 Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp
 305 310 315
 ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aat gtc act gtg 1236
 Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val
 320 325 330
 gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct 1284
 Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala
 335 340 345
 gac tcc ctg ggg cct ctc aaa gac gat gtg cta ctg ttg gag aca cga 1332
 Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg
 350 355 360
 ggc ccc cag gac aac aga tcc ctc tgt gcc ttg gaa ccc agt ggc tgt 1380
 Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys
 365 370 375 380
 act tca cta ccc agc aaa gcc tcc acg agg gca gct cgc ctt gga gag 1428
 Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu
 385 390 395
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 Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
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 Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
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 Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
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 Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
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Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
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Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
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Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp 305 310 315		
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Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
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Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
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Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
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Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
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Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
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 aaywsnathc cnwsntgytg ggcnytnccn tggytnaayg tnwsngcnga yggngayaay 660
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Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro
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Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu	
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Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile	
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His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser	
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Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	Glu	Leu	Leu						
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Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	Trp	Asn	Asp	Asp	Asn						
		415					420					425									
Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	Arg	Arg						
	430					435					440										
Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Phe						
445					450					455					460						
Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Ser						
				465				470						475							
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09863012 052301

490

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ytntggggayg gngaygtnyt ntgyytnccn ggnwsnytn arwsngcncc nggnccngtn 180
ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gyccncaraa racngaytgy 240
gcnytnctgyg tnmngntngt ngtncayytn gcngtncaayg gncaytgggc ngarccngar 300
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gargcnggna arwsngayws ngarytnicar garwsnmgna aygcwnsnyt ncargcncar 360
 gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn 420
 ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar 480
 gcwnsnytn gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar 540
 ytnaayytna encarcaryt nccngaytgy mgnggnytn argtnmgnga ywsnathcar 600
 wsntgytggg tnytnccntg gytnaaygt wsnacngayg gngayaaygt nytnytnacn 660
 ytngaygtw sngargarca rgayttywsn ttyytnytnt ayytnmgnc ngtncngay 720
 gcnytnaarw snytntggta yaaraayytn acnggncnc araayathac nytnaaycay 780
 acngayytn tncntgyyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840
 gtngarttyt gycnttymg ngargayccn ggngcncaym gnaayytn gcyathgcn 900
 mgnytnmgng tnytnwsncc nggngtntgg carytngayg cncntgytg yytnccnggn 960
 aargtnacny tntgytggca rgcncngay carwsnccnt gycarccnyt ngtnccnccn 1020
 gtncncara araaygcnc ngtnaaygar ccncargayt tycarytngt ngcnggncay 1080
 ccnaayytn gygtncargt nwsnacntgg garaargtnc arytncargc ntgyytnagg 1140
 gcngaywsny tnggncntt yaargaygay atgytnytng tngaratgaa racnggnytn 1200
 aayaayacnw sngtntgygc nytngarccn wsnggntgya cncnytncc nwsnatggcn 1260
 wsnacnmng cngcnmgnyt nggngargar ytnytnargc ayttymgnws ncaycartgy 1320
 atgcarytn ggaaygayga yaayatgggn wsnytnagg cntgyccnat ggayaartay 1380
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 ytnwsncara tgccnytnmg ngtngcngtn gayytnaggw snmgngnga rytwnsngcn 1620
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 ttyytnargc gnmngcnac nggngntay gtnggngtnt ayttgyaygg nytnytnacay 1860
 ccngaywsng tncnwsncc nttymgngtn gcncnytn tywsnytncc nwsncarytn 1920
 ccngcnttyy tngaygcnyt ncarggnggn tgywsnacnw sngcnggngm nccngcngay 1980
 mgngtnargm gngtnacna rcnytnmgn wsnycnytn aywsntgyac nwsnwsnwsn 2040
 gargcncng gntgytgyga rgartgggay ytnngncnt gyacnacnyt ngar 2094

09863818 "052301

<210> 13
 <211> 2786
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>

<221> CDS

<222> (70)..(2283)

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<222> (118)..(2283)

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<221> misc_feature

<222> (9)..(134)

<223> Xaa translation (9, 18,26, 109,120, 134) depends
 on genetic code

<400> 13

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cgcacggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111
      Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val
          -15                -10                -5

aac gcc tgc ctc aac ggc tcg cag ctg gct gtn gcc gct ggc ggg tcc 159
Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser
      -1  1                5                10

ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca 207
Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro
      15                20                25                30

gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat 255
Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn
          35                40                45

tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc 303
Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala
          50                55                60

cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc 351
Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val
          65                70                75

acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga 399
Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly
          80                85                90

ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga cag ngc caa 447
Phe Arg Val Ile Leu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln
          95                100                105                110

caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga 495

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Gln	Leu	Ile	Leu	Lys	Asp	Pro	Lys	Gln	Xaa	Asn	Ser	Ser	Phe	Lys	Arg		
				115					120					125			
act	gga	atg	gaa	tct	caa	cct	ttt	ctg	aat	atg	aaa	ttt	gaa	acg	gat	543	
Thr	Gly	Met	Glu	Ser	Gln	Pro	Xaa	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp		
			130					135					140				
tat	ttc	gta	agg	ttg	tcc	ttt	tcc	ttc	att	aaa	aac	gaa	agc	aat	tac	591	
Tyr	Phe	Val	Arg	Leu	Ser	Phe	Ser	Phe	Ile	Lys	Asn	Glu	Ser	Asn	Tyr		
		145					150					155					
cac	cct	ttc	ttc	ttt	aga	acc	cga	gcc	tgt	gac	ctg	ttg	tta	cag	ccg	639	
His	Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro		
	160					165					170						
gac	aat	cta	gct	tgt	aaa	ccc	ttc	tgg	aag	cct	cgg	aac	ctg	aac	atc	687	
Asp	Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile		
175					180					185					190		
agc	cag	cat	ggc	tcg	gac	atg	cag	gtg	tcc	ttc	gac	cac	gca	ccg	cac	735	
Ser	Gln	His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His		
				195				200					205				
aac	ttc	ggc	ttc	cgt	ttc	ttc	tat	ctt	cac	tac	aag	ctc	aag	cac	gaa	783	
Asn	Phe	Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu		
			210					215					220				
gga	cct	ttc	aag	cga	aag	acc	tgt	aag	cag	gag	caa	act	aca	gag	atg	831	
Gly	Pro	Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Met		
		225					230					235					
acc	agc	tgc	ctc	ctt	caa	aat	gtt	tct	cca	ggg	gat	tat	ata	att	gag	879	
Thr	Ser	Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu		
	240					245					250						
ctg	gtg	gat	gac	act	aac	aca	aca	aga	aaa	gtg	atg	cat	tat	gcc	tta	927	
Leu	Val	Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu		
255					260					265					270		
aag	cca	gtg	cac	tcc	ccg	tgg	gcc	ggg	ccc	atc	aga	gcc	gtg	gcc	atc	975	
Lys	Pro	Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile		
				275				280					285				
aca	gtg	cca	ctg	gta	gtc	ata	tcg	gca	ttc	gcg	acg	ctc	ttc	act	gtg	1023	
Thr	Val	Pro	Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val		
			290					295					300				
atg	tgc	cgc	aag	aag	caa	caa	gaa	aat	ata	tat	tca	cat	tta	gat	gaa	1071	
Met	Cys	Arg	Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	Ser	His	Leu	Asp	Glu		
		305				310						315					
gag	agc	tct	gag	tct	tcc	aca	tac	act	gca	gca	ctc	cca	aga	gag	agg	1119	
Glu	Ser	Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu	Arg		
		320				325					330						
ctc	cgg	ccg	cgg	ccg	aag	gtc	ttt	ctc	tgc	tat	tcc	agt	aaa	gat	ggc	1167	
Leu	Arg	Pro	Arg	Pro	Lys	Val	Phe	Leu	Cys	Tyr	Ser	Ser	Lys	Asp	Gly		
335					340				345					350			
cag	aat	cac	atg	aat	gtc	gtc	cag	tgt	ttc	gcc	tac	ttc	ctc	cag	gac	1215	

09863818 052304

Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
 355 360 365
 ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa gac ttc agc ctc 1263
 Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
 370 375 380
 tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag atc cac gag tcc 1311
 Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser
 385 390 395
 cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag tac ttt gtg gac 1359
 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
 400 405 410
 aag aag aac tac aaa cac aaa gga ggt ggc cga ggc tcg ggg aaa gga 1407
 Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly
 415 420 425 430
 gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa aag ctc cgc cag 1455
 Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln
 435 440 445
 gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt atc gcc gtc tac 1503
 Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr
 450 455 460
 ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc cta gac ctg agt 1551
 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser
 465 470 475
 acc aag tac aga ctc atg gac aat ctt cct cag ctc tgt tcc cac ctg 1599
 Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu
 480 485 490
 cac tcc cga gac cac ggc ctc cag gag ccg ggg cag cac acg cga cag 1647
 His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln
 495 500 505 510
 ggc agc aga agg aac tac ttc cgg agc aag tca ggc cgg tcc cta tac 1695
 Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr
 515 520 525
 gtc gcc att tgc aac atg cac cag ttt att gac gag gag ccc gac tgg 1743
 Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp
 530 535 540
 ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca ctg cgc tac cgg 1791
 Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg
 545 550 555
 gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt tta aat gat gtc 1839
 Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val
 560 565 570
 atg tgc aaa cca ggg cct gag agt gac ttc tgc cta aag gta gag gcg 1887
 Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala
 575 580 585 590
 gct gtt ctt ggg gca acc gga cca gcc gac tcc cag cac gag agt cag 1935

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Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln
595 600 605

cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt 1983
His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly
610 615 620

agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa gcc ggc agc ccc 2031
Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro
625 630 635

tcg gac atg ccg cgg gac tca ggc atc tat gac tcg tct gtg ccc tca 2079
Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
640 645 650

tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg acg gac cag aca 2127
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr
655 660 665 670

gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct tca ggc ctg ggt 2175
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly
675 680 685

gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc tct tct ggg tca 2223
Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser
690 695 700

tgc aaa gca gat ctt ggt tgc cgc agc tac act gat gaa ctc cac gcg 2271
Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala
705 710 715

gtc gcc cct ttg taacaaaacg aaagagtcta agcattgccca ctttagctgc 2323
Val Ala Pro Leu
720

tgccctccctc tgattcccca gctcatctcc ctgggttgcag ggcccacttg gagctgaggt 2383

ctcatacaag gatatttgga gtgaaatgct ggccagtact tggtctccct tgccccaacc 2443

ctttaccgga tatcttgaca aactctccaa ttttctaaaa tgatatggag ctctgaaagg 2503

catgtccata aggtctgaca acagcttgcc aaatttggtt agtccttgga tcagagcctg 2563

ttgtgggagg tagggaggaa atatgtaaag aaaaacagga agatacctgc actaatcatt 2623

cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683

gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743

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<211> 738
<212> PRT
<213> Unknown

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Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser Gly Arg
 1 5 10 15
 Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro Ala Ser
 20 25 30
 Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
 35 40 45
 Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
 50 55 60
 Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
 65 70 75 80
 Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
 85 90 95
 Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln Gln Leu
 100 105 110
 Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg Thr Gly
 115 120 125
 Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
 130 135 140
 Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr His Pro
 145 150 155 160
 Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn
 165 170 175
 Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln
 180 185 190
 His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe
 195 200 205
 Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro
 210 215 220
 Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser
 225 230 235 240
 Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val
 245 250 255
 Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro
 260 265 270
 Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val
 275 280 285
 Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys
 290 295 300
 Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser
 305 310 315 320

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Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg
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 Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn
 340 345 350
 His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys
 355 360 365
 Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg
 370 375 380
 Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe
 385 390 395 400
 Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys
 405 410 415
 Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu
 420 425 430
 Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys
 435 440 445
 Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp
 450 455 460
 Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys
 465 470 475 480
 Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser
 485 490 495
 Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser
 500 505 510
 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
 515 520 525
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
 530 535 540
 Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro
 545 550 555 560
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys
 565 570 575
 Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val
 580 585 590
 Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly
 595 600 605
 Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala
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 Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp
 625 630 635 640

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Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala
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Pro Leu

<210> 15
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<213> reverse translation

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<222> (1)..(2214)
<223> n may be a, c, g, or t

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tggnnnggng tnggncngc nwsnmgnaay wsnggnytn tnaayathac nttyaartay 180
gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240
athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300
ggngcnytn gnatgartt yytnaarggn ttymngntna thytnngarga rytnaarwsn 360
garggngmc arnnncarca rytnathytn aargayccna arcarnnnaa ywsnwsntty 420
aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480
gtngmnytnw snttywsntt yathaaraay garwsnaayt aycayccntt yttyttymgn 540
acnmngcngt gygayytnyt nytnarcen gayaayytn cngtgyaarcc nttytggaar 600
ccnmgnaay tnaayathws ncarcayggn wsngaytgc argtnwsntt ygaycaygn 660
ccncayaayt tyggnttymg nttyttytay ytncaytaya arytnaarca ygarggncn 720
ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytnar 780
aaygtnwsnc cnggngayta yathathgar ytngtngayg ayacnaayac nacnmgnaar 840
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<220>
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Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
-5 -1 1 5	
cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
10 15 20 25	
ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
30 35 40	
gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt	240
Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
45 50 55	
cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga	288
Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
60 65 70	
aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
75 80 85	
cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
90 95 100 105	
aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac	432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
110 115 120	
ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc	480
Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
125 130 135	
ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac	528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
140 145 150	
agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg	576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	
155 160 165	
ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag	624
Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu	
170 175 180 185	
gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg	672
Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Leu	
190 195 200	

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agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta	720
Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val	
205 210 215	
gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc	768
Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser	
220 225 230	
tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc	816
Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser	
235 240 245	
tgg cca gaa gcc tat ggc tgc gac ttc tgg aag tca gtg cac ttc act	864
Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr	
250 255 260 265	
gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc	912
Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys	
270 275 280	
cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc	960
Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr	
285 290 295	
ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg	1008
Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp	
300 305 310	
tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta	1056
Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val	
315 320 325	
caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac	1104
Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His	
330 335 340 345	
cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc	1152
Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala	
350 355 360	
cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt	1200
Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser	
365 370 375	
gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc	1248
Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro	
380 385 390	
gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg	1296
Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp	
395 400 405	
aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg	1344
Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu	
410 415 420 425	
atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc	1392
Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala	
430 435 440	

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<210> 17
<211> 657
<212> PRT
<213> Unknown
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<400> 17
Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile
          -20          -15          -10
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Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro
 -5 -1 1 5
 His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro
 10 15 20 25
 Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly
 30 35 40
 Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys
 45 50 55
 Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg
 60 65 70
 Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys
 75 80 85
 Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg
 90 95 100 105
 Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp
 110 115 120
 Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val
 125 130 135
 Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn
 140 145 150
 Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu
 155 160 165
 Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu
 170 175 180 185
 Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu
 190 195 200
 Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val
 205 210 215
 Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser
 220 225 230
 Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser
 235 240 245
 Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr
 250 255 260 265
 Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
 270 275 280
 Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
 285 290 295
 Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
 300 305 310

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Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
 315 320 325
 Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
 330 335 340 345
 Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
 350 355 360
 Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
 365 370 375
 Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
 380 385 390
 Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
 395 400 405
 Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
 410 415 420 425
 Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
 430 435 440
 Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
 445 450 455
 Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
 460 465 470
 Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
 475 480 485
 Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
 490 495 500 505
 Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
 510 515 520
 Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
 525 530 535
 Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
 540 545 550
 Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
 555 560 565
 Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
 570 575 580 585
 Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
 590 595 600
 Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
 605 610 615
 Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
 620 625 630

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Gly

<210> 18
 <211> 1971
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1971)
 <223> n may be a, c, g, or t

<400> 18
 atgggnwsnw snmgnytngc ngcnytnytn ytncncytny tnytnathgt nathgayytn 60
 wsngaywsng cnggnathgg nttymgncay ytncncayt ggaayacnmg ntgyccnytn 120
 gcnwsncaya cngargtnyt nccnathwsn ytngcngcnc cnggnggncc nwsnwsnccn 180
 carwsnytn gngtntgyga rwsnggnacn gtncngcng tntgygcnws nathtgytgy 240
 cargtngcnc argtnttyaa yggngcnwsn wsnacnwsnt ggtgymgnaa yccnaarwsn 300
 ytncncayw snwsnwsnat hggngayacn mgntgyccarc ayytnytnmg nggnwsntgy 360
 tgyytngtng tnacntgyyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420
 ccnacnmng aytygcnyt naarggnccn ayytnmgna thcarmgna yggnaargtn 480
 ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmgntgggtn 540
 carytnwsng gnggncnga rtywsntty gayytnytn cngargcnmg ngcnathmgn 600
 gtnacnathw snwsnggncc ngargtnwsn gtnmgnytn gycaycartg ggcnytngr 660
 tgygargary tnwsnwsncc ntaygaygtn caraarathg tnwsnggngg ncayacngtn 720
 garytnccnt aygarttyyt nytnccntgy ytntgyathg argcnwsnta yytnccargar 780
 gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargenta yggnwsngay 840
 ttytggaarw sngtnaytt yacngaytay wsnarcaya cncaratggt natggcnyn 900
 acnytnmgnt gyccnytnaa rytngargcn gcnytntgyc armgncayga ytggcayacn 960
 ytntgyaarg ayytnccnaa ygcnacngcn mgngarwsng ayggntggta ygtnytngr 1020
 aargtngayy tncayccna rytntgytty aargtnccarc cntgggtyws nttyggnaay 1080
 wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtwnsnatg 1140
 gayacncarg cncarcaryt nathytnay ttywsnwsnm gnatgcaygc nacnttywsn 1200
 gcngcntggw snytnccngg nytnngncar gayacnytn tncncncgt ntayacngtn 1260
 wsnargtn ggmgnwsnga ygtncartty gcntggaarc ayytnytn gcnaygtn 1320

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wsntaymgnc ayytnggny nytnathytn gcnytnytny cnytnytnac nytnytnngn 1380
 gtngtnytny cnytnacntg ymgngmgncn carwsnggnc cnggncngc nmgnccngtn 1440
 ytnytnytnc aygngcnga ywsngargcn carmgngny tngtnggngc nytnngcngar 1500
 ytnytnmgng cngcnytnng nggnggngmgn gaygtathg tngayytny ggarggngmgn 1560
 caygtngcnm gngtnggnc nytnccntg ytntgggng cnmgnacnmg ngtnngcnmgn 1620
 garcarggna cngtnytny nytnnggwn ggngcngayy tnmgnccngt nwsnggncn 1680
 gayccnmng cngcncny nytnngcnytn ytnaygng cncncmgnc nytnytnytn 1740
 ytnngcntayt tywsnmgny ntgygcnaar ggngayathc cncncncny nmngcnytn 1800
 ccnmngntaym gnytnytnm ngayytnccn mgnytnytnm gngcnytna ygcnmgnccn 1860
 ttygcngarg cnacnwsntg gggngmgnytn ggngcnmgnc armngmgna rwsnmgnytn 1920
 garytnygyw snmgnytna rmngargcn gcnmgnytn cngayytnng n 1971

<210> 19
 <211> 808
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:rodent; surmised
 Mus musculus

<220>
 <221> CDS
 <222> (78)..(806)

<220>
 <221> mat_peptide
 <222> (147)..(806)

<400> 19
 cagctccggg ccagccctg ctgccctctt gcagacagga aagacatggt ctctgcgccc 60
 tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
 -20 -15
 tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
 Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
 -10 -5 -1 1
 tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206
 Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
 5 10 15 20
 gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254
 Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
 25 30 35
 gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302

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Val Arg Lys Ser Lys Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His
 40 45 50

agg aca cca gca tcc ttc cag agg aag ctg cta ggc agc cct tcc ctg 350
 Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu
 55 60 65

tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac 398
 Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His
 70 75 80

aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga 446
 Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg
 85 90 95 100

gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc 494
 Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe
 105 110 115

tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct 542
 Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro
 120 125 130

gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa 590
 Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu
 135 140 145

tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga 638
 Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly
 150 155 160

ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc 686
 Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys
 165 170 175 180

ata gag gcc tcc tac ctg caa gag gac act gtg agg cgc aaa agt gtc 734
 Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val
 185 190 195

cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa 782
 Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln
 200 205 210

tac gct tca ctg act aca gcc agc ac 808
 Tyr Ala Ser Leu Thr Thr Ala Ser
 215 220

<210> 20
 <211> 243
 <212> PRT
 <213> Unknown

<400> 20
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 -20 -15 -10

Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
 -5 -1 1 5

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Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 10 15 20 25
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 30 35 40
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 45 50 55
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 60 65 70
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 75 80 85
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 90 95 100 105
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 110 115 120
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
 125 130 135
 Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 140 145 150
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
 155 160 165
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
 170 175 180 185
 Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly
 190 195 200
 Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr
 205 210 215
 Thr Ala Ser
 220

<210> 21
 <211> 729
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(729)
 <223> n may be a, c, g, or t

<400> 21
 atgggnwsnc cnmgnytngc ngcnytnytn ytnwsnytn cnytnytnytn nathggnytn 60
 gcngtnwsng cnmgngtngc ntgyccntgy ytnmgntwsnt ggacnwsnca ytggytnytn 120
 gcntaymgng tngayaarmg nttygcnggn ytncartggg gntgggttycc nytnytnngtn 180

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mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn 240
 ttycarmgna arytnytngg nwsnccnwsn ytnwsngarg arwsncaymg nathwsnath 300
 ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngcngcn 360
 garggnmgng arcayytncc ngargcnggn wsncaraart gyggnggncc ngarttywsn 420
 ttygayytny tncngargt ncargcngtn mgngtnacna thccngcngg nccnaargcn 480
 mgngtnmgny tntgytayca rtgggcnyn tn gartgygarg ayytnwsnws nccnttygay 540
 acncaraara thgtnwsngg nggncayacn gtngayytnc cntaygartt yytnytnccn 600
 tgyatgtgya thgargcnws ntayytnear gargayacng tnmgnmgnaa rwsngtnccn 660
 wsnmgngcng gnytnaaryt natggcncar acnwsnggnw sncartaygc nwsnytnacn 720
 acngcnwsn 729

<210> 22
 <211> 2377
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (180)..(1874)

<400> 22
 ttttgagcag aggtctccta ggctccgtag aaatttgcat acagcttcca ctctctgctt 60
 cagagcctgt tcttctactt acctgggccc ggagaagggtg gagggagacg agaagccgcc 120
 gagagccgac taccctccgg gccagtcctg tctgtccgtg gtggatctaa gaaactaga 179
 atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca 227
 Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
 1 5 10 15
 agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca 275
 Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
 20 25 30
 gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct 323
 Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
 35 40 45
 gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac 371
 Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
 50 55 60
 tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc 419
 Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
 65 70 75 80

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acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc 467
 Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
 85 90 95

agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca 515
 Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
 100 105 110

gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag 563
 Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
 115 120 125

cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag 611
 His Gln Phe Ser Phe Met Gln Lys Arg Asn Gln Trp Leu Val Ser Gln
 130 135 140

ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac 659
 Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
 145 150 155 160

caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag 707
 Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
 165 170 175

atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg 755
 Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
 180 185 190

cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc 803
 Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
 195 200 205

atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc 851
 Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
 210 215 220

cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa 899
 Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
 225 230 235 240

cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc 947
 Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
 245 250 255

cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat 995
 Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
 260 265 270

cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa 1043
 His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
 275 280 285

gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg 1091
 Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
 290 295 300

aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc 1139
 Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
 305 310 315 320

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tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg 1187
 Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
 325 330 335

ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct 1235
 Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
 340 345 350

ggt gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag 1283
 Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
 355 360 365

gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac 1331
 Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
 370 375 380

cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg 1379
 Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
 385 390 395 400

cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg 1427
 Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
 405 410 415

aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac 1475
 Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
 420 425 430

ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag 1523
 Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
 435 440 445

cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc 1571
 Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
 450 455 460

aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat 1619
 Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
 465 470 475 480

gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag 1667
 Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
 485 490 495

ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc 1715
 Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
 500 505 510

cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat 1763
 Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
 515 520 525

gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg 1811
 Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
 530 535 540

aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt 1859
 Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
 545 550 555 560

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cag gtg gtt ccc ttg tgacaccggt catccccaga tcaactgaggc caggccatgt 1914
Gln Val Val Pro Leu
565

ttggggcctt gttctgacag cattctggct gaggetggtc ggtagcactc ctggctgggt 1974
tttttctgtt cctccccgag aggcctctg gccccagga aacctgttgt gcagagctct 2034
tccccggaga cctccacaca ccttggcttt gaagtggagt ctgtgactgc tctgcattct 2094
ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttctctct gacagtttga 2154
tgtgtccatt ctgggcctct cagtgetttag caagtagata atgtaaggga tgtggcagca 2214
aatggaaatg actacaaaca ctctctatc aatcatttca ggctactttt atgagtttagc 2274
cagatgcttg tgtatcttca gaccaaactg attcatgtac aaataataaa atgtttactc 2334
ttttgtaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2377

<210> 23
<211> 565
<212> PRT
<213> Unknown

<400> 23

Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
1 5 10 15

Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
20 25 30

Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
35 40 45

Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
50 55 60

Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
65 70 75 80

Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
85 90 95

Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
100 105 110

Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
115 120 125

His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
130 135 140

Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
145 150 155 160

Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
165 170 175

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Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
 180 185 190
 Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
 195 200 205
 Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
 210 215 220
 Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
 225 230 235 240
 Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
 245 250 255
 Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
 260 265 270
 His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
 275 280 285
 Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
 290 295 300
 Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
 305 310 315 320
 Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
 325 330 335
 Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
 340 345 350
 Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
 355 360 365
 Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
 370 375 380
 Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
 385 390 395 400
 Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
 405 410 415
 Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
 420 425 430
 Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
 435 440 445
 Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
 450 455 460
 Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
 465 470 475 480
 Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
 485 490 495

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Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
500 505 510

Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
515 520 525

Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
530 535 540

Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
545 550 555 560

Gln Val Val Pro Leu
565

<210> 24

<211> 1695

<212> DNA

<213> reverse translation

<220>

<221> misc_feature

<222> (1)..(1695)

<223> n may be a, c, g, or t

<400> 24

atgaaymgw snathccngt ngargtngay garwsngarc cntayccnws ncarytynytn 60
aarcenathc cngartayws nccngargar garwsngarc cncngcncc naayathmgn 120
aayatggcnc cnaaywsnyt nwsngcnccn acnatgytnc ayaaywsnws nggngaytty 180
wsncargcnc aywsnacnyt naarytngcn aaycaycarm gncngtnws nmgnrcargtn 240
acntgyytnm gnacncargt nytngargay wsngargayw snttytgymg nmgnrcayccn 300
ggnytnngna argcnttycc nwsnggntgy wsngcngtnw sngarccngc nwsngarwsn 360
gtngtnngng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420
ytngtnwsnc arytnwsngc ngcnwsnccn gayacnggnc aygaywsnga yaarwsngay 480
carwsnytn cnaaygcnws ngcngaywsn ytnngnggnw sncargarat ggtnrcarmgn 540
cncarcnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600
wsncarcnc argaygtnyt nggnathmgn carytngarm gncnytncc nytnacnwsn 660
gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720
ccncarmgnt aycngcntg ygcncaratg ytnccncna ayytnwsncc ncaygcncn 780
tggaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840
tayccnmng cngcntayca rcargtnath carccngcny tncnggnca rccnytnccn 900
ggngcnwsng tnmnggnytn ncayccngtn caraargtna thytnaayta yccnwsnccn 960

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tgggaycarg argarmgncc ngcncarmgn gaytgywsnt tyccnggnyt nccnmgnca 1020
 cargaycarc cncaycayca rccnccnaay mgngcnggng cncnggnga rwsnytngr 1080
 tgyccngcng arytnmgnc ncartnccn carcnccnw snccngcngc ngtnccnmgn 1140
 ccccnwsna ayccncngc nmngngnacn ytnaaracnw snaayytnc ngargarytn 1200
 mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260
 ttyytntyng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320
 athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380
 gcnathwsnc cnaartayaa rcargaygtn garggngcng arwsncaryt ngaygargay 1440
 garcayggny tncayacnaa rtayathcay mgnatgatgc arathgartt yathaarc 1500
 ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560
 ccnactggy tncaraayac ncaygntay wsntggccna araayaaraa raayathytn 1620
 ytnmgnytny tnmnggarga rgartaygtn gcnccncnm gnggncnyt nccnacnytn 1680
 cargtngtnc cnytn 1695

<210> 25
 <211> 1323
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:rodent; surmised
 Mus musculus

<220>
 <221> CDS
 <222> (1) .. (1026)

<400> 25
 cag gac ctc cct ggg cct ctg agg tcc agg gaa ttg cca cct cag ttt 48
 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1 5 10 15
 gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct 96
 Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30
 tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144
 Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45
 tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192
 Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60
 tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240
 Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

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gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
225 230 235 240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
245 250 255	
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
260 265 270	
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
275 280 285	
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
290 295 300	
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
305 310 315 320	

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ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc 1008
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc 1056
 Leu Gln Val Val Pro Leu
 340

ctgttctcac agcattcttc tagcggagct ggctggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcctgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc 1296

tcaaataata aaatgattat tctttgt 1323

<210> 26
 <211> 342
 <212> PRT
 <213> Unknown

<400> 26
 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1 5 10 15

Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30

Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
 85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
 100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
 115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
 130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
 145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
 165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val

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180										185										190										
Val	Lys	Phe	Val	Asn	Phe	Leu	Leu	Val	Asn	Gly	Phe	Gln	Thr	Ala	Ile															
		195					200					205																		
Asp	Ile	Phe	Glu	Asp	Arg	Ile	Arg	Gly	Ile	Asp	Ile	Ile	Lys	Trp	Met															
	210					215					220																			
Glu	Arg	Tyr	Leu	Arg	Asp	Lys	Thr	Val	Met	Ile	Ile	Val	Ala	Ile	Ser															
225					230					235					240															
Pro	Lys	Tyr	Lys	Gln	Asp	Val	Glu	Gly	Ala	Glu	Ser	Gln	Leu	Asp	Glu															
				245					250					255																
Asp	Glu	His	Gly	Leu	His	Thr	Lys	Tyr	Ile	His	Arg	Met	Met	Gln	Ile															
		260						265					270																	
Glu	Phe	Ile	Ser	Gln	Gly	Ser	Met	Asn	Phe	Arg	Phe	Ile	Pro	Val	Leu															
		275					280					285																		
Phe	Pro	Asn	Ala	Lys	Lys	Glu	His	Val	Pro	Thr	Trp	Leu	Gln	Asn	Thr															
	290					295					300																			
His	Val	Tyr	Ser	Trp	Pro	Lys	Asn	Lys	Lys	Asn	Ile	Leu	Leu	Arg	Leu															
305					310					315					320															
Leu	Arg	Glu	Glu	Glu	Tyr	Val	Ala	Pro	Pro	Arg	Gly	Pro	Leu	Pro	Thr															
			325					330					335																	
Leu	Gln	Val	Val	Pro	Leu																									
			340																											

<210> 27
 <211> 1026
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1026)
 <223> n amy be a, c, g, or t

<400> 27
 cargayytnc cnggnccnyt nmgnwsnmgn garytnccnc cncarttyga rytngarmgn 60
 tayccnatga aygcncaryt nytnccnccn cayccnwsnc cncargcncc ntggaaytgy 120
 cartaytayt gycngggngg nccntaycay caycargtnc cncayggncay yggntayccn 180
 ccngcngcng cntaycarca rgtnytnear ccngcnytncc cnggncargt nytnccnggn 240
 gcnmgngcnm gnggnccnmg nccngtnear aargtnathy tnaaygayws nwsnccncar 300
 gaycargarg armgncngc ncarmgngay ttywsnttyc cnmgnytncc nmngngaycar 360
 ytnaymgnc cncnwsnaa yggngtngar gcnccngarg arwsnytnge yytnccngcn 420
 garytnmgnc cncayggnc nccargcnccn wsnytnge cngtnccnmg nccnccnwsn 480

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aayccnytn cnmgnggnac nytnmgnacn wsnaayytnc cngargaryt nmgnaargtn 540
 ttyathacnt aywsnatgga yacngcnatg gargtngtna arttygtnaa yttyytnytn 600
 gtnaayggnt tycaracngc nathgayath ttygargaym gnathmgngg nathgayath 660
 athaartgga tggarmgnta yytnmgngay aaracngtna tgathathgt ngcnathwsn 720
 ccnaartaya arcargaygt ngarggngcn garwsncary tngaygarga ygarcaaygg 780
 ytncaayacna artayathca ymgngatgatg carathgart tyathwsnca rggnwsnatg 840
 aayttymgnt tyathccngt nytnnttyccn aaygcnaara argarcaygt nccnacntgg 900
 ytncaraaya cncaygtnta ywsntggccn aaraayaara araayathyt nytnmgnytn 960
 ytnmgngarg argartaygt ngcnccncn mgnggncny tncnacnyt ncargtngtn 1020
 ccnytn 1026

<210> 28
 <211> 207
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: primate; surmised
 Homo sapiens

<400> 28
 Arg Lys Val Trp Ile Ile Tyr Ser Ala Asp His Pro Leu Tyr Val Asp
 1 5 10 15
 Val Val Leu Lys Phe Ala Gln Phe Leu Leu Thr Ala Cys Gly Thr Glu
 20 25 30
 Val Ala Leu Asp Leu Leu Glu Glu Gln Ala Ile Ser Glu Ala Gly Val
 35 40 45
 Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
 50 55 60
 Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp Gln Ala
 65 70 75 80
 Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His Gly Lys
 85 90 95
 Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp
 100 105 110
 Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser
 115 120 125
 Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala Ala Pro
 130 135 140
 Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln
 145 150 155 160

000033818 052301

Asp Leu Glu Met Phe Gln Pro Gly Arg Met His Arg Val Gly Glu Leu
165 170 175

Ser Gly Asp Asn Tyr Leu Arg Ser Pro Gly Gly Arg Gln Leu Arg Ala
180 185 190

Ala Leu Asp Arg Phe Arg Asp Trp Gln Val Arg Cys Pro Asp Trp
195 200 205

<210> 29

<211> 208

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: rodent; surmised
Mus musculus

<400> 29

Arg Lys Val Trp Ile Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu
1 5 10 15

Val Val Leu Lys Phe Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu
20 25 30

Val Ala Leu Asp Leu Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val
35 40 45

Met Thr Trp Val Ser Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
50 55 60

Lys Ile Ile Ile Leu Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala
65 70 75 80

Ile Leu Gly Trp Ala Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp
85 90 95

Lys Pro Ala Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro
100 105 110

Asp Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe
115 120 125

Ser Gly Ile Cys Ser Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr
130 135 140

Ser Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile
145 150 155 160

Gln Asp Leu Glu Met Phe Glu Pro Gly Arg Met His His Val Arg Glu
165 170 175

Leu Thr Gly Asp Asn Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys
180 185 190

Glu Ala Val Leu Arg Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp
195 200 205

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<210> 30
 <211> 190
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown Organism:worm; surmised
 Caenorabditis elegans

<400> 30

Val Lys Val Met Ile Val Tyr Ala Asp Asp Asn Asp Leu His Thr Asp
 1 5 10 15
 Cys Val Lys Lys Leu Val Glu Asn Leu Arg Asn Cys Ala Ser Cys Asp
 20 25 30
 Pro Val Phe Asp Leu Glu Lys Leu Ile Thr Ala Glu Ile Val Pro Ser
 35 40 45
 Arg Trp Leu Val Asp Gln Ile Ser Ser Leu Lys Lys Phe Ile Ile Val
 50 55 60
 Val Ser Asp Cys Ala Glu Lys Ile Leu Asp Thr Glu Ala Ser Glu Thr
 65 70 75 80
 His Gln Leu Val Gln Ala Arg Pro Phe Ala Asp Leu Phe Gly Pro Ala
 85 90 95
 Met Glu Met Ile Ile Arg Asp Ala Thr His Asn Phe Pro Glu Ala Arg
 100 105 110
 Lys Lys Tyr Ala Val Val Arg Phe Asn Tyr Ser Pro His Val Pro Pro
 115 120 125
 Asn Leu Ala Ile Leu Asn Leu Pro Thr Phe Ile Pro Glu Gln Phe Ala
 130 135 140
 Gln Leu Thr Ala Phe Leu His Asn Val Glu His Thr Glu Arg Ala Asn
 145 150 155 160
 Val Thr Gln Asn Ile Ser Glu Ala Gln Ile His Glu Trp Asn Leu Cys
 165 170 175
 Ala Ser Arg Met Met Ser Phe Phe Val Arg Asn Pro Asn Trp
 180 185 190

<210> 31
 <211> 178
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown Organism:worm; surmised
 Caenorabditis elegans

00003010 0000301

<400> 31

Phe Lys Val Met Leu Val Cys Pro Glu Val Ser Gly Arg Asp Glu Asp
 1 5 10 15

Phe Met Met Arg Ile Ala Asp Ala Leu Lys Lys Ser Asn Asn Lys Val
 20 25 30

Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met
 35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val
 50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
 65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
 85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
 100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
 115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
 130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
 145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
 165 170 175

Asn Ser

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